AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1-91 (Cancelled)

92. (NEW) A method for analyzing a polynucleotide, comprising:

a) providing a polynucleotide having homology to a defined DNA sequence;

b) calculating the masses of two or more polypeptides encoded in two or more reading frames of said defined DNA sequence thereby obtaining a set of predicted mass values;

c) expressing two or more polypeptides from two or more reading frames of said polynucleotide, thereby creating two or more expressed polypeptides;

d) measuring the masses of said two or more expressed polypeptides, thereby obtaining a set of observed mass values; and

e) comparing said set of predicted mass values to said set of observed mass values..

93. (NEW) The method of claim 92, wherein the polynucleotide contains a difference with respect to the defined DNA sequence and wherein said difference is selected from the group consisting of single nucleotide polymorphism, single nucleotide substitution, single nucleotide deletion, single nucleotide insertion, multiple nucleotide substitution, multiple nucleotide deletion, multiple nucleotide insertion, DNA duplication, DNA inversion, DNA translocation, and DNA deletion/substitution.

94. (NEW) The method of claim 92, wherein the polynucleotide comprises an exon.

95. (NEW) The method of claim 92, wherein the polynucleotide comprises a cDNA.

96. (NEW) The method of claim 92, wherein the polynucleotide comprises at least one predetermined epitope tag.

97. (NEW) The method of claim 92, wherein the expressed polypeptides are expressed in a living cell.

98. (NEW) The method of claim 92, wherein the expressed polypeptides are expressed in a cell free system.

99. (NEW) The method of claim 92, wherein said cell free system is selected from the group consisting of E. coli extract, rabbit reticulocyte extract, and wheat germ extract.

100. (NEW) The method of claim 92, further comprising purification of the polypeptide prior to measuring its measured peptide mass signature.

101. (NEW) The method of claim 100, wherein said purification comprises a method selected from the group consisting of gel electrophoresis, capillary electrophoresis, liquid

chromatography (LC), capillary liquid chromatography, high performance liquid chromatography (HPLC), differential centrifugation, filtration, gel filtration, membrane chromatography, affinity purification, biomolecular interaction analysis (BIA), ligand affinity purification, glutathione-S-transferase affinity chromatography, cellulose binding protein affinity chromatography, maltose binding protein affinity chromatography, avidin/streptavidin affinity chromatography, S-tag affinity chromatography, thioredoxin affinity chromatography, metal-chelate affinity chromatography, immobilized metal affinity chromatography, epitope-tag affinity chromatography, immunoaffinity chromatography, immunoaffinity capture, capture using bioreactive mass spectrometer probes, mass spectrometric immunoassay, and immunoprecipitation.

102. (NEW) The method of claim 92 wherein the polypeptide masses are measured by a method selected from the group consisting of mass spectrometry, MALDI-TOF mass spectrometry, electrospray ionization mass spectrometry (ESI), tandem mass spectrometry (MS/MS), quadripole time of flight spectrometry (Q-TOF), Fourier transform ion cyclotron resonance (FTICR) mass spectrometry, gel electrophoresis, capillary electrophoresis, and high performance liquid chromatography (HPLC).